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FIG. 1-1

Set
h

V _H 4-39		D6-13		J _H 5		N		W		F		D				
C	A	R	H/Q	TGT	GCG	AGA	CA					AAC	TGG	TTC	GAC	
C	A	S	R	TGT	GCG	AGC	TCC	AGA	GGG	TAT	AGC	AGC	TGG	TAC	Y	
C	A	R	H	TGT	GCG	AGA	CAT	CTG	GGG	TAT	AGC	AGC	TGG	TAC	W	
C	A	R	R	TGT	GCG	AGA	CAG	TAT	GGG	TAT	AGC	AGC	TGG	TAC	Y	
C	A	R	F	TGT	GCG	AGA	CGG	TTC	GGG	TAT	AGC	AGC	TGG	TAC	W	
C	A	R	S	T	G	G	A	S	S	S	S	S	TAC	Y		
C	A	R	Q	TGT	GCG	AGG	TGC	ACC	GGG	TAT	AGC	AGC	TGG	TAC	W	
C	A	R	H	E	TGT	GCG	AGA	CAA	GCT	GGG	TAT	AGC	AGC	TGG	TAC	Y
C	A	R	H	E	TGT	GCG	AGA	CAT	GAG	GGG	TAT	AGC	AGC	TGG	TAC	---

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FIG. 1-2

Set II.

V _H 4-34	D5-5	J _H 6
C A R G Y D T A M V AT TAC TAC TAC	GTC GAT ACA GCT ATG GTT AC	
TGT GCG AGA GGATAC GGG GAT ACA CCT ACC ATT AGA AGA TAC TAT	P V F R Y Y	CLL183
C A R G Y A D T A M V AT TAC TAC TAC	GTC GAT ACA GCT ATG GTT AC	
TGT GCG AGA GGATAC GGG GAT ACA CCT ACC ATT AGA AGA TAC TAT	P V F R Y Y	CLL240
C A R G W G D T A M V AT TAC TAC TAC	GTC GAT ACA GCT ATG GTT AC	
TGT GCG AGA GGCG TGG GGG GAT ACA CCT ACC ATT AGA AGA TAC TAC	P M L K R Y Y	CLL342
C A R A Y P D T A M V AT TAC TAC TAC	GTC GAT ACA CCT ATG GTC AGG AGG TAC TAC	AF087422 CLL 4B 1
TGT GCG AGA GCA TAC CCG GAT ACA CCT ATG GTC AGG AGG TAC TAC	D V I K R Y Y	
C A R G F P D T A M V AT TAC TAC TAC	GTC GAT ACA CCT ATG GTC AGG AGG TAC TAC	AJ239333 CLL 1D 47
TGT GCG AGA GGC TTC CCG GAT ACA GAT GTC ATT AAG CGC TAC TAC		

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FIG. 1 - 3

Set VIa.

	V _H 1-02	D6-19	J _H 4
C	A R D/E		Y F D Y
TGT GCG AGA GA		AC TAC TTT GAC TAC	
V	Q	W	L V
GG <u>GTA</u> TAG CAG TGG CTG <u>GTA</u> C	L V	L E	H Y
TGT GCG AGG GAG CAG TGG CTG <u>GTA</u> CTT GAG CAC TAC TTT GAC TAC	L E	F D	Y
C A R V Q W L R	-	H F D	Y
TGT GCG AGA GTG CAG TGG CTG <u>GTC</u> TTA AGA ---	G L	N F D	Y
C A R E Q W L G A	-	CAC TTT GAC TAC	
TGT GCG AGA GAG CAG TGG CTG GCC GCA GAA ---	G A	E	
C A R E Q W L V L K	-	N F D	Y
TGT GCG AGG GAG CAG TGG CTG <u>GTA</u> AAA ---	G C	E	
C A R V Q W L L E	-	AAC TTT GAC TAC	
TGT GCG AGA GTT CAG TGG TTA TTA CTC GAA ---	G C	R F D	Y
C A R N Q W L G D	-	CGA TTT GAC TAC	
TGT GCG AGA AAC CAG TGG CTG GGT CTC ---	G L	Y F D	Y
C A R E Q W L V R T	-	GAC TAC TTT GAC TAC	
TGT GCG AGA GAG CAG TGG CTG <u>GTA</u> AGG ACG ---	G V	S F D	Y
		AGC TTT GAC TAC	
		U86787	CLL-H2B 1 U0
		AJ239371	CLL 3 2
		AJ487492	SMZL Tiereins, A.M. U3

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FIG. 1 - 4

Set VIB,c,d

V _{b1} -03	D6-19	J _{H4}
C A R D/E	TGT GCG AGA GA	Y F D Y
V <u>GTA</u> TAG CAG	Q <u>TGG</u> CTG GTAC	W <u>L</u> V
<u>GG</u>	<u>GTA</u>	<u>GTC</u> <u>GTA</u> C
C A R E Q W L V S - Y F D Y	TGT GCG AGG GAG CAG TGG CTG GTC CTA TCT --- TAC TTT GAC TAC CLL336	C A R E Q W L V L - N Y F D Y
C A R E Q W L V GAG CAG TGG CTG GTC CTA TCT --- AAC TAC TTT GAC TAC CLL360	TGT GCG AGA GAG CAG TGG CTG GTC CTA AAA --- CCC TTT GAC TAC AF376961 LAN Digheiro	C A R K Q W L A I V N Y F D Y
TGT GCG AGA AAC CAG TGG CTG GCC ATC GTC AAC TAC TTT GAC TAC L01278 CLL-412 ³	TGT GCG AGA AAC CAG TGG CTG GCC ATC GTC AAC TAC TTT GAC TAC L01278 CLL-412 ³	TGT GCG AGA AAC CAG TGG CTG GTC CTA CCT --- ACC TTT GAC TAC U86801 ⁴ U3/1
C A R V Q W L G L T G P - T F D Y	TGT GCT AGG GTT CAG TGG CTG GGC CTG ACG GGG CCG AAT GAC TAC U84176 KEM (VHL-46) ⁵ U0	C A R G Q W L V I L - N F D Y
TGT GCG AGG GGA CAG TGG CTG GTC ATC CTA --- AAC TTT GAC TAC U84162 BYR (VHL-46) ⁵ U0	TGT GCG AGA GAT CAG TGG CTG CCC ACG --- AAC AAC TTT GAC TAC AF376953 Digheiro PIQ U2	TGT GCG AGG GAC CAG TGG TTG GTC CTA CCT --- CAC TTT GAC TAC CLL154 (VHL-18)

FIG. 1 - 5

Set IV.

V _H 1-69			D3-16			J _H 3													
C	A	R	D/E	TGT	GCG AGA GA	G	TAT	TAC	GAT	TAC	GTT	TGG	GCG	AGT	TAT	CGT	TAT	ACC	
C	A	R	G	G	D	Y	D	Y	V	V	W	G	S	Y	R	S	R	Y	
TGT	GCG	AGA	GGA	GGC	GAT	TAT	GAT	TAC	GTT	TGG	GGG	AGT	TAT	CGT	ICT	AAT	GAT	GCT	
C	A	R	G	G	I	Y	D	Y	W	W	G	S	Y	R	P	N	D	F	
TGT	GCG	AGA	GGA	GGG	GGT	ATT	TAT	GAT	TAC	GTT	TGG	GGG	AGT	TAT	CGT	CCG	AAT	GAT	GCT
C	A	R	G	G	N	Y	D	Y	I	W	G	S	Y	R	S	N	D	A	
TGT	GCG	AGA	GGA	GGC	AAT	TAT	GAT	TAC	ATT	TGG	GGG	AGT	TAT	CGT	ICC	AAT	GAT	GCT	TTT
C	A	R	G	G	D	Y	D	Y	V	W	G	S	Y	R	P	N	D	A	
TGT	GCG	AGA	GGA	GGG	GGG	GAT	TAT	GAT	TAC	GTT	TGG	GGG	AGT	TAT	CGT	CCG	AAT	GAT	GCT
C	A	R	G	G	N	Y	D	Y	I	W	G	S	Y	R	S	N	D	A	
TGT	GCG	AGA	GGA	GGC	AAT	TAT	GAT	TAC	ATT	TGG	GGG	AGT	TAT	CGT	ICC	AAT	GAT	GCT	TTT

D
A
F
D
I
T
GAT
GCT
TTT
GAT
GTC

Martin, France

α-cardiolipin

CLL068

CLL258

CLL022 Russia

AJ414008

AAC51720

CLL SMI⁵

AF460965 α-cardiolipin

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FIG. 1 - 6

Set V.

V _H 1-69	D3-10			J _H 5																
C	A	R	D/E	I	T	M	V	R	G	V	I	I	G	I	Y	Y	AT	TAC	TAC	TAC
TGT GCG AGA GA				GT	ATT	ACT	ATG	GTT	CGG	GGA	GTT	ATT	ATA	AC						
C A E G M V Q G V I G I Y Y				TGT GCG GAG GCT ATG GTT CAG GGA GTT ATT GGA ATT TAC TAC													AJ389179	GN12	8	
C A R S M V Q G V I N V L Y Y				TGT GCG AGG TCT ATG GTT CAG CGA GTT ATT AAC GTC CTC TAC TAC													AAC51697	FUH	5	
C A R A M V R G V I H L D Y Y				TGT GCG AGG GCT ATG GTT CGG GGA GTT ATT CAC TTG GAC TAC TAC													AJ239372	ID64	2	
TGT GCG AGA GTT ATG GTT CGG GGA GTT ATT TCC CTG GAC TAC TAC																		AF376959	SIN Dicheiro	UO

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FIG. 1 - 7

Set III.

V _H 3-21	J _H 6
C A R D E/D	
TGT GCG AGA GA	
Y Y Y Y	
AT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC	
C A R D A N G M D V W G	
TGT GCG AGA GAT GCG AAT GGA ATG GAC GTC TGG GGC	CLL282
C A R D R N G M D V W G	
TGT GCG AGA GAT CGG AAC GGT ATG GAC GTC TGG GGC	CLL175
C A R D Q N G M D V W G	
TGT GCG AGA GAT CAA AAC GGT ATG GAC GTC TGG GGC	CLL412
C A S D R N G M D V W G	
TGT GCG AGC GAT CGA AAC GGT ATG GAC GTC TGG GGC	AJ239379 ID28 ²
C A R E P Y G M D V W G	
TGT GCG AGA GAG CCA TAC GGT ATG GAC GTC TGG GGC	AF174100 sc77u-16 ⁹
C A R D G S G M D V W G	
TGT GCG AGA GAT GGC TCC GGT ATG GAC GTC TGG GGC	AJ389178 GN11 ⁸
C A R D A N G M D V W G	
TGT GCG AGA GAT GCT AAC GGC ATG GAC GTC TGG GGC	AF299104 IF case 10 ¹⁰ U3

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FIG. 1-8

Set Vie

V _H 5-51		D6-19		J _H 4	
C	A	R	Q/H	Y	F
TGT	GCG	AGA	CA	AC	TAC
V	—	Q	W	TTT	GAC
GG	GTA	TAG	CAG	TGG	TAC
C	A	R	Q	L	V
TGT	GCG	AGG	CAG	G	D
C	A	R	Q	G	F
TGT	GCG	AGA	AGG	CTG	TTT
C	A	R	Q	G	G
TGT	GCG	AGA	CAG	GGC	CAC
C	A	R	Q	G	T
TGT	GCG	AGA	CAG	TGG	TAC
C	A	R	Q	G	Y
TGT	GCG	AGA	CAG	TTC	GTC
C	A	R	Q	G	Y
TGT	GCG	AGA	CAG	TGG	TAC
C	A	R	E	G	F
TGT	GCG	AGA	GAG	TCA	ACT
C	A	R	Q	W	L
TGT	GCG	AGA	CAG	TGG	GTC
C	A	R	E	W	L
Not available					

FIG. 1 - 9

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V _{H1-02}	D ₆₋₁₉	J _{H4}
C A R D/E TGT GCG AGA GA	V Q W L V GG GTA TAG CAG TGG CTG GTA C	F D Y AC TTT GAC TAC
C A R E Q W L V L E H Y F D Y TGT GCG AGG GAG CAG TGG CTG GTA CTT GAG CAC TAC TTT GAC TAC CLL011	C A R V Q W L G L R - H F D Y TGT GCG AGA GTG CAG TGG CTG GCC TTA AGA --- CAC TTT GAC TAC CLL270	C A R E Q W L G A E - N F D Y TGT GCG AGA GAG CAG TGG CTG GGC GCA GAA --- AAC TTT GAC TAC CLL266
C A R E Q W L V L K - N F D Y TGT GCG AGG GAG CAG TGG CTG GTA CTG AAA --- AAC TTT GAC TAC CLL340	C A R V Q W L L L E - R F D Y TGT GCG AGA GTT CAG TGG TTA TTA CTC GAA --- CGA TTT GAC TAC AJ239371 CLL 3 ²	C A R N Q W L G L D - Y F D Y TGT GCG AGA AAC CAG TGG CTG GGT CTC GAC --- TAC TTT GAC TAC AJ487492 SMZL Tierens, A.M.
C A R E Q W L V R T - S F D Y TGT GCG AGA GAG CAG TGG CTG GTA AGG ACG --- AGC TTT GAC TAC U86787 CLL-H2B ¹ U0	C A R E Q W L V L S - Y F D Y TGT GCG AGG GAG CAG TGG CTG GTC CTA TCT --- TAC TTT GAC TAC CLL336	C A R E Q W L A L K - P F D Y TGT GCG AGA GAG CAG TGG CTG GCC TTA AAA --- CCC TTT GAC TAC AF376961 LAN Digheiro
C A R K Q W L A I V N Y F D Y TGT GCG AGA AAG CAG TGG CTG GCC ATC GTC AAC TAC TTT GAC TAC L01278 CLL-412 ³	C A R E Q W L G L P - T F D Y TGT GCG AGA GAG CAG TGG CTG GGT CTA CCT --- ACC TTT GAC TAC U86801 ⁴ U3/1	TGT GCT AGG GTT CAG TGG CTG GGC CTG ACG GGG CCG AAT GAC TAC U84176 KEM (VH1-46) ⁵ U0
C A R G Q W L V I L - N F D Y TGT GCG AGG GGA CAG TGG CTG GTC ATC CTA --- AAC TTT GAC TAC U84162 BYR (VH1-46) ⁵ U0	C A R D Q W L P T - N N F D Y TGT GCG AGA GAT CAG TGG CTG CCC ACG --- AAC AAC TTT GAC TAC AF376953 Digheiro PIQ U2	C A R E Q W L V L S - H F D Y TGT GCG AGG GAG CAG TGG TTG GTA CTA TCT --- CAC TTT GAC TAC CLL154 (VH1-18)
C A R Q Q W L G G D Y F D Y TGT GCG AGG CAG CAG TGG CTG GGT GGC GAC TAC TTT GAC TAC CLL026	C A R R Q W L A L G H F D Y TGT GCG AGA AGG CAG TGG CTG GCC CTA GGC CAC TTT GAC TAC AF099198 Tre ¹¹ 012/0-2	JK2
C A R Q Q W F G V TGT GCG AGA CAG CAA TGG TTC GGC GTG C A R Q Q W L V L TGT GCG AGA CAG CAG TGG CTG GTA CTT C A R E Q W L I V TGT GCG AGA GAG CAG TGG CTC ATA GTA C A R Q Q W L V L TGT GCG AGA CAG CAG TGG CTG GTG TTG	Y Y F D Y TAC TAC TTT GAC TAC AJ414007 CLL021 Russia U0 P Y F D Y CCA TAC TTT GAC TAC AJ239373 ID38 ² T H F D Y ACT CAC TTT GAC TAC AJ555263 GO14 D Y F D Y GAC TAC TTT GAC TAC AJ272398 AG ¹² S N F D Y Not available PH1562 HOW ¹³	

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FIG. 2

Amino acid alignments of the H chain variable regions of all sequences in each Set

	CDR1	CDR2	CDR3
Set IV			
Germline	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARD	YYDLYWGGSYRYDAFDVWQGQGMVTVSS	
MCLL068	GGD.....SN.....
MCLL258	GGL.....PN.....
MF9	GGP.....PN.....
SMI	GGN...I.....SN.....
CLL022	E.....
RIZ	GGD.....PN.....I
Consensus	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARGGDDYDVNGSYRXXNADPDIWQGGMVTVSS	GGN...I.....SN.....V.....	
Set VIII			
Germline	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARD	YYDLYWGGSYRYDAFDVWQGQGMVTVSS	CDR3
FS41	GD.....AS.....
UCA4	E.....GA.....EG.....
GO13	E.....E.....TR.....
Consensus	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARGGDDYDVNGSYRXXNADPDIWQGGMVTVSS	GGG.....V.....	
Set V			
Germline	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARD	YYDLYWGGSYRYDAFDVWQGQGMVTVSS	CDR3
CLL561	E.....AM.Q...QTY...Y...K.....
MJ21	A.....Y.....X.....K.....
RP22	G.....Y.....Y.....K.....
GN12	EG...Q...GI.....
F0H	E.....S.Q...NVL.....
ZD64	E.....A.....BLD.....X.....
SIN	E.....V.....SLD.....Y.....X.....L.....
Consensus	QVQLVQSGAEVKPGSSVKVSKASGGTFSYYAISWVRQAPGQGLEWNGGIPIFGTANYAQRQGRVTITADKSTSTAYMELSSLRSEDATAVYTCARXOMVRGVITKYYYYYMDVWQGKGTIVTVSS	GGG.....V.....	
Set XII			
Germline	QVQLQWQAGLKKPSETSLTCAVYGGSFSGYIYNSWIRQPPKGLEWIGETINHGSTYINPSLSKRSRVTSVDTSKNQFSLKLSSVTAADTAVYTCARG	VTDAMVYYYDLYWGGSYRYDAFDVWQGQGMVTVSS	CDR3
CLL183
CLL240
CLL342
CLL44B
ID47
Consensus	QVQLQWQAGLKKPSETSLTCAVYGGSFSGYIYNSWIRQPPKGLEWIGETINHGSTYINPSLSKRSRVTSVDTSKNQFSLKLSSVTAADTAVYTCARG	YDTPMXRRYYYYMDVWQGKGTIVTVSS	
Set VIA			
Germline	QVQLVQSGAEVKPGASVKVSKASGYTFPTSYAMHWRQAPGQGLEWNGWINDNGGTTYQRFQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCARD	QNLV.....YFDYWGQGTLVTVSS	CDR3
CLL011	E.....LEH.....
CLL266	E.....GAEN.....
CLL270	V.....GLRH.....
CLL340	S.....LHN.....
CLL3	V.....LLER.....
SLV18	N.....GLD.....
CLL-H2B	E.....RTS.....
Consensus	QVQLVQSGAEVKPGASVEVKASGYTFPTSYAMHWRQAPGQGLEWNGWINDNGGTTYQRFQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCAREQWLLEN	YFDYWGQGTLVTVSS	
Set VIIb			
Germline	QVQLVQSGAEVKPGASVKVSKASGYTFPTSYAMHWRQAPGQGLEWNGWINDNGGTTYQRFQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCARD	YFDYWGQGTLVTVSS	CDR3
CLL336	E.....LS.....
LAN	E.....L.....
CLL-412	E.....ALK-P.....
POR	K.....RIVN.....
PTQ	E.....GLP-T.....
Consensus	QVQLVQSGAEVKPGASVEVKASGYTFPTSYAMHWRQAPGQGLEWNGWINDNGGTTYQRFQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCAREQWLLEN	BTM-N.....	
Set VIC			
Germline	QVQLVQSGAEVKPGASVKVSKASGYTFPTSYAMHWRQAPGQGLEWNGWINDNGGTTYQRFQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCARD	YFDYWGQGTLVTVSS	CDR3
CLL154	G.....E.....LSH.....
Set Vid			
Germline	QVQLVQSGAEVKPGASVKVSKASGYTFPTSYAMHWRQAPGQGLEWNGIINFSGGTYAQRQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCARD	YFDYWGQGTLVTVSS	CDR3
BXR
KSM
Consensus	QVQLVQSGAEVKPGASVKVSKASGYTFPTSYAMHWRQAPGQGLEWNGIINFSGGTYAQRQGRVTITRDTSTSTAYMELSSLRSEDATAVYTCARQWXXXXXXEDYWQGTLVTVSS	VGLIGPN.....	
Set VIe			
Germline	EVQLVQSGAEVKPGESLRISCKGGTYSFTSYAMHWRQMPGKLEWNGRIDPSDGYINPSFQGHVTISADKSISTAYLQNSSLRASTDAMYTICARQNLV	YFDYWGQGTLVTVSS	CDR3
CLL026	GGD.....
TRB	E.....ALCH.....
CLL021	PGVY.....
ID36	LP.....
GO14	IVTH.....
AG	LD.....
HOW	E.....ESN.....
Consensus	EVQLVQSGAEVKPGESLRISCKGGTYSFTSYAMHWRQMPGKLEWNGRIDPSDGYINPSFQGHVTISADKSISTAYLQNSSLRASTDAMYTICARQNLV	YFDYWGQGTLVTVSS	

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FIG. 3

Amino acid alignments of the L chain variable regions of all sequences in each Set.

<i>Set IV</i>		<u>CDR1</u>	<u>CDR2</u>	<u>CDR3</u>
Germeline	ERTLTQSPGTLSLSGERATLSCRASQSSSYLAWYQQKPGQAPHLITYGASSRATDIPDRFSGSGCDFTLTISLEPEDFAVYTCQQYGSSTPFGQGTKEIK			
CLL068			
CLL258			
MF9			
Consensus	ERTLTQSPGTLSLSGERATLSCRASQSSSYLAWYQQKPGQAPHLITYGASSRATDIPDRFSGSGCDFTLTISLEPEDFAVYTCQQYGSSTPFGQGTKEIK			
<i>Set VIII</i>		<u>CDR1</u>	<u>CDR2</u>	<u>CDR3</u>
Germeline	EVLTQSPATLISPGERATLSCRASQSSSYLAWYQQKPGQAPHLITYGASSRATDIPDRFSGSGCDFTLTISLEPEDFAVYTCQQYGSSTPFGQGTKEIK			
Go13			
<i>Set V</i> -		<u>CDR1</u>	<u>CDR2</u>	<u>CDR3</u>
Germeline	QSVLTQPPASGTPGQRTVTIACGSSSNIGSNTNTYQQLGTAPKKLIVSNQRPBGTDRFGSKSGTSAASLAISCLOSED			
RF12			
GN12			
Consensus	QSVLTQPPASGTPGQRTVTIACGSSSNIGSNTNTYQQLGTAPKKLIVSNQRPBGTDRFGSKSGTSAASLAISCLOSED			
<i>Set I</i>		<u>CDR1</u>	<u>CDR2</u>	<u>CDR3</u>
Germeline	DVATATQSPISLPLPVTLGQPASITSCRSSQPSIVYEDNTVLYNFFQQRPGQSPRLILYKVSNTUDSGVYDREFGSGSGDFTLKISRVEADYCAWDDSLNGKXFFGGTKEIK			
CLL183			
CLL240			
CLL342			
Consensus	DVATATQSPISLPLPVTLGQPASITSCRSSQPSIVYEDNTVLYNFFQQRPGQSPRLILYKVSNTUDSGVYDREFGSGSGDFTLKISRVEADYCAWDDSLNGKXFFGGTKEIK			
<i>Set VI</i>		<u>CDR1</u>	<u>CDR2</u>	<u>CDR3</u>
Consensus	DIQMTOSPSSL6ASVYGDRTVITCRASQSSSYLAWYQQKPGQAPHLITYGASSRATDIPDRFSGSGCDFTLTISLEPEDFAVYTCQQYGSSTPFGQGTKEIK			
CLL011			
CLL266			
CLL270			
CLL340			
CLL346			
CLL350	F		
CLL-412			
CLL154			
TRP			
Go14			
Consensus	DIQMTOSPSSL6ASVYGDRTVITCRASQSSSYLAWYQQKPGQAPHLITYGASSRATDIPDRFSGSGCDFTLTISLEPEDFAVYTCQQYGSSTPFGQGTKEIK			

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FIG. 4

V _H 1-69	D3-16	J _H 3	D A F D I	V _K 227	J _K 1/4*5*
C A R D/E tgt ggg aga ga	Y Y D Y V W G S Y R Y g tat tat gag tac gtt tgg ggg agt tat cgt tat acc	t gat gct ttg gat acc	cag cgg tat ggt agc tca ctc cc	Q Q Y G S S P P W T F G	g tgg acg tcc ggc
G G D	S N	CLL068	P N	CLL258	
ga ggc g...	ga a...	cg...	
G G I	I	P N	G
gg ggt at...	g...
G G P	S N	P N	P
ga ggg cc...	cg...	
G G N	I	S N	
ga ggc a...	cc...	g... #
G G D	I	P N	
gg ggg g...	cg...	
G G N	I	S N	CLL022 (natural Ab producing clone)
ga ggg a...	cc...	α -cardiolipin
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22					1 2 3 4 5 6 7 8 9 10 11

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FIG. 5

V _H 1-69	D2-2	J _H 6	V _{KL} 6	J _K 3
C A R D/E		Y Y	Q Q	P P
tgt gcg aga ga	D I V V P A A I	at tac tac	cag cgt aac tgg cct cc	F T F G P G
ag gag att gta gta cca gct gct ata cc			a ttc act ttc ggc cct ggg	
• • G G	• • • • M S	- - -	FS41	
• • . gg ggc	•	g t.c		
• • G A	•	M G	- - -	UCA4
• • G G	•	M R	- - -	G013
• . . gg.	g .ga	•
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18			1 2 3 4 5 6 7 8 9 10	

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FIG. 6

V _H 1-69	D3-10	J _H 6	V _L 1-16	W D D S L N G P	J _L 1/3*
C A R D/E		Y Y Y			
tgt gcg aga ga		at tac tac tac		tgg gat gac agc ctg aat ggt cc	
I I M V R G V T I				Y V F G	
gt att act atg gtt cgg sga gtt att ata ac				t tgg gtg ttc ggc	
• • A • Q • Q T • •	• • Q • Q T • •	CLL561	• • T Y • •	RF22	• • R • •
• •	•	•	•	•	•
• • A • • • • • •	• • T Y • • •	MJ21	•	•	•
• •	•	•	•	•	•
• • G • • • • • •	•	•	•	•	•
• •	•	•	•	•	•
• • E G • • Q • •	•	•	•	•	•
• • sag g	•	•	•	•	•
• • S • • Q • • •	•	•	•	•	•
• •	•	•	•	•	•
• • A • • • • • •	•	•	•	•	•
• •	•	•	•	•	•
• • V • • • • • •	•	•	•	SIN	
• •	•	•	•		
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15					
				1 2 3 4 5 6 7 8 9 10 11	

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FIG. 7

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FIG. 8

V _H 1-02	D6-19	J _H 4	V _K 012/02	J _K 1/2*
C A R D / E		Y F D Y	Q Q S Y S T P P	
tgt gcg aga ga		ac tao ttt gac tac	caa cag agt tac agt acc ect cc	
V * Q W L V				W T F G
gg gta tag cag tgg otg gta o				g tgg acg tto ggc
.	L E H . . .	CLL011	.	T
.	G A E - N . . .	CLL266	.	- K . . .
.	V . . . G L R - H . . .	CLL270	.	
.	L K - N . . .	CLL340	.	
.	V . . . L L E - R . . .	CLL3	.	
.	N . . . G L D . . .	slv18 (marginal zone lymphoma)	.	
.	E . . . R T - S . . .	CLL-H2B	.	
.	L S - . . .	CLL336	.	S . . .
.	L - N . . .	CLL360	.	
.	A L K - P . . .	LAN	.	
.	K . . . A I V N . . .	CLL-412	.	
.	P T - N N . . .	PTQ	.	
.	L S - H . . .	CLL154	.	
.	G . . . I L - N . . .	BYR	.	
.	V . . . G L T G P N . . .	KEM	.	
.	G G - D . . .	CLL026	.	
.	R . . . A L - G H . . .	TRE	.	
.	F G V - Y . . .	CLL021	.	
.	L P - . . .	ID38	.	
.	E . . . I V T - H . . .	GO14	.	- R . . .
.	L - D . . .	AG	.	agg . . .
.	E . . . L S - . . .	HOW		
nucleotide sequence not available				
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15			1 2 3 4 5 6 7 8 9 10 11 12 13	